

RAW SEQUENCE LISTING

DATE: 04/03/2001

PATENT APPLICATION: US/09/695,121

TIME: 12:46:33

Input Set : A:\US09695121.raw

Output Set: N:\CRF3\04032001\I695121.raw

C--> 1 <110> APPLICANT: Gilbertson, Debra G.
2 <120> TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
3 <130> FILE REFERENCE: 00-53
4 <140> CURRENT APPLICATION NUMBER: US/09/695,121
5 <141> CURRENT FILING DATE: 2001-04-03
6 <160> NUMBER OF SEQ ID NOS: 18
7 <170> SOFTWARE: FastSEQ for Windows Version 3.0
9 <210> SEQ ID NO: 1
10 <211> LENGTH: 1760
11 <212> TYPE: DNA
12 <213> ORGANISM: Homo sapiens
13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (154)...(1191)
16 <400> SEQUENCE: 1

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18	agtgcagcct tcccctggcg gtggtgaaag agactcggga gtcgctgctt ccaaagtgcc	120
19	cgccgtgagt gagctctcac ccagtcagc caa atg agc ctc ttc ggg ctt ctc	174
20		
21		
22	ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa	222
23	Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu	
24	10 15 20	
25	tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac	270
26	Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn	
27	25 30 35	
28	gga gta caa gat cct cag cat gag aga att att act gtg tct act aat	318
29	Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn	
30	40 45 50 55	
31	gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg	366
32	Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr	
33	60 65 70	
34	gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa	414
35	Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln	
36	75 80 85	
37	ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata	462
38	Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile	
39	90 95 100	
40	tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata	510
41	Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile	
42	105 110 115	
43	tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct	558
44	Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser	
45	120 125 130 135	
46	aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct	606
47	Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro	
48	140 145 150	

ENTERED

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49	tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc	654
50	Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe	
51	155 160 165	
52	aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg	702
53	Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu	
54	170 175 180	
55	gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt	750
56	Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu	
57	185 190 195	
58	att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta	798
59	Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu	
60	200 205 210 215	
61	tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga	846
62	Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg	
63	220 225 230	
64	aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta	894
65	Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu	
66	235 240 245	
67	tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta	942
68	Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu	
69	250 255 260	
70	aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc	990
71	Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg	
72	265 270 275	
73	tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa	1038
74	Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln	
75	280 285 290 295	
76	tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg	1086
77	Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu	
78	300 305 310	
79	aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg	1134
80	Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val	
81	315 320 325	
82	gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca	1182
83	Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr	
84	330 335 340	
85	gga gga tag ccgcacacc accagcagct cttgccaga gctgtgcagt	1231
86	Gly Gly *	
87	345	
88	gcagtggctg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt	1291
89	gcttcaagga cctttcatct tcaggattta cagtgcattc tgaaagagga gacatcaaac	1351
90	agaattagga gttgtgcaac agctcttttg agaggaggcc taaaggacag gagaaaagg	1411
91	cttcaatcgt ggaaagaaaa ttaaatgttg tattaatatag atcaccagct agtttcagag	1471
92	ttaccatgta cgtattccac tagctgggtt ctgtatttca gttctttcga tacggcttag	1531
93	ggtaatgtca gtacaggaaa aaaactgtgc aagtgcagcac ctgattccgt tgccttgctt	1591
94	aactctaaag ctccatgtcc tgggcctaaa atcgtataaa atctggattt ttttttttt	1651
95	tttttgctca tattcacata tgtaaacag aacattctat gtactacaaa cctgggtttt	1711
96	aaaaaggaac tatgttgcta tgaattaaac ttgtgtcgtg ctgatagga	1760
98	<210> SEQ ID NO: 2	

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99 <211> LENGTH: 345
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
103 Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
104 1 5 10 15
105 Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
106 20 25 30
107 Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
108 35 40 45
109 Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
110 50 55 60
111 His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
112 65 70 75 80
113 Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
114 85 90 95
115 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
116 100 105 110
117 Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
118 115 120 125
119 Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
120 130 135 140
121 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
122 145 150 155 160
123 Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
124 165 170 175
125 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
126 180 185 190
127 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
128 195 200 205
129 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
130 210 215 220
131 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
132 225 230 235 240
133 Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
134 245 250 255
135 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
136 260 265 270
137 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
138 275 280 285
139 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
140 290 295 300
141 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
142 305 310 315 320
143 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
144 325 330 335
145 Cys Val Cys Arg Gly Ser Thr Gly Gly
146 340 345
148 <210> SEQ ID NO: 3

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/695,121

DATE: 04/03/2001

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Input Set : A:\US09695121.raw

Output Set: N:\CRF3\04032001\I695121.raw

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149 <211> LENGTH: 3571
150 <212> TYPE: DNA
151 <213> ORGANISM: Mus musculus
152 <220> FEATURE:
153 <221> NAME/KEY: CDS
154 <222> LOCATION: (1049)...(2086)
155 <400> SEQUENCE: 3
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157   ggcggcattctcgcgcgcagtggtgggtctgtctgcgcggggccgcagtgccccctgt    120
158   ctgcgccagcacctgttgccgcgcagctggccgcgcgcgcgcgcgcgcgcgcgcgcgcgc    180
159   cgcccgccgcgcagcccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc    240
160   ggggacaaga gcatcctccaggccagcca ggccttcccttagccgcgcgcgcgcgcgcgc    300
161   ccacctctctcagccctgcgtcctgccctgccttagggcaggcatccgagcgtcgcga    360
162   ctccgagccg cccaagctctcccggtctccgcagcacttcgccggtaccgcagggaact    420
163   tcggtggcca ccgactgcagcaaggaggaggtccgcgcgtggatccgggcagtcgccgag    480
164   tcgtcccccgcggcctctctgcgcgcgcgggacccgcgcgcgcactcgcagggcacgggtccc    540
165   ctccccccaggtgggggtggggcgccgcctgccgcccga tcagcagctt tgcattgat    600
166   cccaaggtgc tcgcctcgtgccgacctggcttcagcttggtggcgaccccgagt    660
167   cctcgctgtgtcctgtccc caaaactgacagggtgctccc tgcgagtcgc cagcactcat    720
168   cgccgtccc ccgcgtcccc acccttcttctctccctgc cctacccccccccccgcac    780
169   ttccggcacagctcaggattt gtttaaaccttgggaaactggttcaggtcc aggttttgct    840
170   ttgatccttt tcaaaaactg gagacacaga agagggtctc aggaaaaact ttgggatggg    900
171   attatgtgga aactaccctgcgattctctgctgccagagc cggccaggcgcttcaccgc    960
172   agcgcagcct ttcccgggtgggctgagcc ttggagtgtcgcttccccgtgcccgccg    1020
173   cgagtgagcc ctcgcccagtcagccaa atgctctctcggcctctctc    1072
174                                     Met Leu Leu Leu Gly Leu Leu Leu
175                                     1             5
176   ctgaca tctgccctggc caaaga acggg actcgg gctgag tcc    1120
177   Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser
178   10             15             20
179   aacctg agcagc aagttg cagctc tccagc gac aag gaa cag aac gga    1168
180   Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly
181   25             30             35             40
182   gtgcaa gatccc cggcat gaggaga gttgtc actata tctggt aatggg    1216
183   Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly
184   45             50             55
185   agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg    1264
186   Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val
187   60             65             70
188   ctggtg tggaga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg    1312
189   Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu
190   75             80             85
191   aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc    1360
192   Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys
193   90             95             100
194   aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta    1408
195   Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu
196   105            110            115            120
197   gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa    1456
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198	Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys	
199	125 130 135	
200	gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct	1504
201	Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser	
202	140 145 150	
203	gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca	1552
204	Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr	
205	155 160 165	
206	gaa acc acg agt cct tgc gtg ttg ccc cct tca tct ttg tca ttg gac	1600
207	Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp	
208	170 175 180	
209	ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att	1648
210	Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile	
211	185 190 195 200	
212	cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac	1696
213	Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr	
214	205 210 215	
215	aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa	1744
216	Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys	
217	220 225 230	
218	agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac	1792
219	Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr	
220	235 240 245	
221	agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag	1840
222	Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys	
223	250 255 260	
224	agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt	1888
225	Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys	
226	265 270 275 280	
227	gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt	1936
228	Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys	
229	285 290 295	
230	gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga	1984
231	Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg	
232	300 305 310	
233	cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct	2032
234	Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala	
235	315 320 325	
236	ctg gaa cac cac gag gaa tgt gac tgt gtg tgt aga gga aac gca gga	2080
237	Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Asn Ala Gly	
238	330 335 340	
239	ggg taa ctgcagcctt cgtagcagca cagctgagca ctggcattct gtgtaccccc	2136
240	Gly *	
241	345	
242	acaagcaacc ttcattcccca ccagcgttgg ccgcagggt ctcagctgct gatgctggct	2196
243	atggtaaaga tcttactcgt ctccaaccaa attctcagtt gtttgettca atagccttcc	2256
244	cctgcaggac ttcaagtgtc ttctaaaaga ccagaggcac caagaggagt caatcacaaa	2316
245	gcactgcctt ctagaggaag ccagacaat ggtcttctga ccacagaaac aaatgaaatg	2376
246	aatgtagatc gctagcaaac tctggagtga cagcatttct tttccactga cagaatgggt	2436

VERIFICATION SUMMARY

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L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date

STATISTICS SUMMARY

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Input Set : A:\US09695121.raw

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Application Serial Number: US/09/695,121

Alpha or Numeric: Numeric

Application Class:

Application File Date: 04-03-2001

Art Unit:

Software Application: FastSeq

Total Number of Sequences: 18

Total Nucleotides: 5655

Total Amino Acids: 1060

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 1

MESSAGE SUMMARY

271 C: 1 (Current Filing Date differs)